

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: RADIN, DAVID N.
CRAMER, CAROLE L.
OISHI, KAREN K.
WEISSENBERN, DEBORAH L.
- (ii) TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
PLANT-BASED EXPRESSION SYSTEMS
- (iii) NUMBER OF SEQUENCES: 12
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Pennie & Edmonds
 - (B) STREET: 1155 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: USA
 - (F) ZIP: 10036-2711
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/003,737
 - (B) FILING DATE: 14-SEP-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Coruzzi, Laura A.
 - (B) REGISTRATION NUMBER: 30,742
 - (C) REFERENCE/DOCKET NUMBER: 7956-0011-999
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 790-9090
 - (B) TELEFAX: (212) 869-9741
 - (C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTGTCTAGAG TAAGCATCAT GGCTGGC

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CACGAATTCT GGCGACGCCA CAGGTAGGTG TGA

33

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGAGTTTT CAAGTCCTTC CAGAGAGGAA TGTCCCAAGC CTTTGAGTAG GGTAAGCATC	60
ATGGCTGGCA GCCTCACAGG TTGCTTCTA CTTCAGGCAG TGTCGTGGGC ATCAGGTGCC	120
CGCCCCTGCA TCCCTAAAAG CTTGCGCTAC AGCTCGGTGG TGTGTGTCTG CAATGCCACA	180
TACTGTGACT CCTTTGACCC CCCGACCTTT CCTGCCCTTG GTACCTTCAG CCGCTATGAG	240
AGTACACGCA GTGGGCGACG GATGGGGCTG AGTATGGGGC CCATCCAGGC TAATCACACG	300
GGCACAGGCC TGCTACTGAC CCTGCAGCCA GAACAGAAGT TCCAGAAAGT GAAGGGATTT	360
GGAGGGGCCA TGACAGATGC TGCTGCTCTC AACATCCTTG CCCTGTCACC CCCTGCCCCA	420
AATTTGCTAC TTAAATCGTA CTTCTCTGAA GAAGGAATCG GATATAACAT CATCCGGGTA	480
CCCATGGCCA GCTGTGACTT CTCCATCCGC ACCTACACCT ATGCAGACAC CCCTGATGAT	540
TTCCAGTTGC ACAACTTCAG CCTCCAGAG GAAGATACCA AGCTCAAGAT ACCCCTGATT	600
CACCGAGCCC TGCAGTTGGC CCAGCGTCCC GTTTCCTCC TTGCCAGCCC CTGGACATCA	660
CCCCTTGGC TCAAGACCAA TGGAGCGGTG AATGGGAAGG GGTCCTCAA GGGACAGCCC	720
GGAGACATCT ACCACCAGAC CTGGGCCAGA TACTTTGTGA AGTTCCTGGA TGCCTATGCT	780
GAGCACAAGT TACAGTTCTG GGCAGTGACA GCTGAAAATG AGCCTTCTGC TGGGCTGTTG	840
AGTGGATACC CCTTCCAGTG CCTGGGCTTC ACCCCTGAAC ATCAGCGAGA CTTCATTGCC	900
CGTGACCTAG GTCCTACCCT CGCCAACAGT ACTCACCACA ATGTCCGCCT ACTCATGCTG	960
GATGACCAAC GCTTGCTGCT GCCCACTGG GCAAAGGTGG TACTGACAGA CCCAGAAGCA	1020

GCTAAATATG TTCATGGCAT TGCTGTACAT TGGTACCTGG ACTTTCTGGC TCCAGCCAAA 1080
 GCCACCCTAG GGGAGACACA CCGCCTGTTC CCCAACACCA TGCTCTTTGC CTCAGAGGCC 1140
 TGTGTGGGCT CCAAGTTCTG GGAGCAGAGT GTGCGGCTAG GCTCCTGGGA TCGAGGGATG 1200
 CAGTACAGCC ACAGCATCAT CACGAACCTC CTGTACCATG TGGTCGGCTG GACCGACTGG 1260
 AACCTTGCCC TGAACCCCGA AGGAGGACCC AATTGGGTGC GTAACCTTGT CGACAGTCCC 1320
 ATCATTGTAG ACGTCACCAG GGACACGTTT TACAAACAGC CCATGTTCTA CCACCTTGGC 1380
 CACTTCAGCA AGTTCATTCC TGAGGGCTCC CAGAGAGTGG GGCTGGTTGC CAGTCAGAAG 1440
 AACGACCTGG ACGCAGTGGC ACTGATGCAT CCCGATGGCT CTGCTGTTGT GGTCGTGCTA 1500
 AACCGCTCCT CTAAGGATGT GCCTCTTACC ATCAAGGATC CTGCTGTGGG CTTCTGGAG 1560
 ACAATCTCAC CTGGCTACTC CATTACACCC TACCTGTGGC GTCGCCAGAA TTCGGACTAC 1620
 AAGGACGACG ATGACAAGTT GA 1642

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Glu	Phe	Ser	Ser	Pro	Ser	Arg	Glu	Glu	Cys	Pro	Lys	Pro	Leu	Ser	1	5	10	15
Arg	Val	Ser	Ile	Met	Ala	Gly	Ser	Leu	Thr	Gly	Leu	Leu	Leu	Leu	Gln	20	25	30	
Ala	Val	Ser	Trp	Ala	Ser	Gly	Ala	Arg	Pro	Cys	Ile	Pro	Lys	Ser	Phe	35	40	45	
Gly	Tyr	Ser	Ser	Val	Val	Cys	Val	Cys	Asn	Ala	Thr	Tyr	Cys	Asp	Ser	50	55	60	
Phe	Asp	Pro	Pro	Thr	Phe	Pro	Ala	Leu	Gly	Thr	Phe	Ser	Arg	Tyr	Glu	65	70	75	80
Ser	Thr	Arg	Ser	Gly	Arg	Arg	Met	Glu	Leu	Ser	Met	Gly	Pro	Ile	Gln	85	90	95	
Ala	Asn	His	Thr	Gly	Thr	Gly	Leu	Leu	Leu	Thr	Leu	Gln	Pro	Glu	Gln	100	105	110	
Lys	Phe	Gln	Lys	Val	Lys	Gly	Phe	Gly	Gly	Ala	Met	Thr	Asp	Ala	Ala	115	120	125	
Ala	Leu	Asn	Ile	Leu	Ala	Leu	Ser	Pro	Pro	Ala	Gln	Asn	Leu	Leu	Leu	130	135	140	
Lys	Ser	Tyr	Phe	Ser	Glu	Glu	Gly	Ile	Gly	Tyr	Asn	Ile	Ile	Arg	Val	145	150	155	160

Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp
 165 170 175
 Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp
 180 185 190
 Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln
 195 200 205
 Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu
 210 215 220
 Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro
 225 230 235 240
 Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu
 245 250 255
 Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu
 260 265 270
 Asn Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu
 275 280 285
 Gly Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly
 290 295 300
 Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu
 305 310 315 320
 Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr
 325 330 335
 Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr
 340 345 350
 Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg
 355 360 365
 Leu Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser
 370 375 380
 Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met
 385 390 395 400
 Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly
 405 410 415
 Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp
 420 425 430
 Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Val Thr Lys Asp
 435 440 445
 Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
 450 455 460
 Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys
 465 470 475 480
 Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val
 485 490 495
 Val Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys
 500 505 510
 Asp Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile

515

520

525

His Thr Tyr Leu Trp Arg Arg Gln Asn Ser Asp Tyr Lys Asp Asp Asp
 530 535 540

Asp Lys
 545

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "MeGA Promoter"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CAATACGATA TTACCGAATA TTATACTAAA TCAAAATTTA ATTTATCATA TCAATTATTA	60
AAC TGATATT TCAAAATTTA ATATTTAATA TCTACTTTCA ACTATTATTA CCTAATTATC	120
AAATGCAAAA TGTATGAGTT ATTTTCATAAT AGCCCGAGTTC GTATCCAAAT ATTTTACACT	180
TGACCAGTCA ACTTGACTAT ATAAACTTT ACTTCAAAAA ATTAAAAAAA AAAGAAAAGTA	240
TATTATTGTA AAAGATAATA CTCCATTCAA AATATAAAAT GAAAAAAGTC CAGCGCGGCA	300
ACCGGGTTCC TATAAATACA TTTCTCTACAT CTCTCTCTCT CCTCACATCC CATCACTCTT	360
CTTTTAACAA TTATACTTGT CAATCATCAA TCCCACAAAC AACACTTTTT CTCTCCTCTT	420
TTTCCTCACC GCGGCGCAGAC TTACCGGTGA AAGTAAGCAG STC	463

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTAGTCTAGA ATGCGTCCCC TCGCCCCCG CG

32

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGAATTTCGAG CTCTCATGGA TTGCCCGGGG ATG

33

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2067 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGCGTCCCC TGCGCCCCCG CGCCGCGCTG CTGGCGCTCC TGGCCTCGCT CCTGGCCGCG	60
CCCCCGGTGG CCCCCGCCGA GGCCCGCAC CTGGTGCAGG TGGACGCGGC CCGCGCGCTG	120
TGGCCCCTGC GGCCTTCTG GAGGAGCACA GGCTTCTGCC CCCCCTGCC ACACAGCCAG	180
GCTGACCACT ACGTCCTCAG CTGGGACCAG CAGCTCAACC TCGCCTATGT GGGCGCCGTC	240
CCTCACCGCG GCATCAAGCA GGTCGGGACC CACTGGCTGC TGGAGCTTGT CACCACCAGG	300
GGGTCCACTG GACGGGGCCT GAGCTACAAC TTCACCCACC TGGACGGGTA CTTGGACCTT	360
CTCAGGGAGA ACCAGCTCCT CCCAGGGTTT GAGCTGATGG GCAGCGCCTC GGGCCACTTC	420
ACTGACTTTG AGGACAAGCA GCAGGTGTTT GAGTGAAGG ACTTGGTCTC CAGCCTGGCC	480
AGGAGATACA TCGGTAGGTA CGGACTGGCG CATGTTTCCA AGTGGAAGTT CGAGACGTGG	540
AATGAGCCAG ACCACCACGA CTTTGACAAC GTCTCCATGA CCATGCAAGG CTTCTGAAC	600
TACTACGATG CCTGCTCGGA GGGTCTGCGC GCCGCCAGCC CCGCCCTGCG GCTGGGAGGC	660
CCCGGCGACT CCTTCCACAC CCCACCGCGA TCCCCGCTGA GCTGGGGCCT CCTGCGCCAC	720
TGCCACGACG GTACCAACTT CTTCACTGGG GAGGCGGGCG TGCGGCTGGA CTACATCTCC	780
CTCCACAGGA AGGGTGCGCG CAGCTCCATC TCCATCCTGG AGCAGGAGAA GGTCTGTCGCG	840
CACGAGATCC GGCAGCTCTT CCCCAAGTTC GCGGACACCC CCATTTACAA CGACGAGGCG	900
GACCCGCTGG TGGGCTGGTC CCTGCCACAG CCGTGGAGGG CGGACGTGAC CTACGCGGCC	960
ATGGTGGTGA AGGTCATCGC GCAGCATCAG AACCTGCTAC TGGCCAACAC CACCTCCGCC	1020
TTCCCCTACG CGCTCCTGAG CAACGACAAT GCCTTCCTGA GCTACCACCC GCACCCCTTC	1080
GCGCAGCGCA CGCTCACCAG GCGCTTCCAG GTCAACAACA CCCGCCCGCC GCACGTGCAG	1140
CTGTTGCGCA AGCCGGTGCT CACGGCCATG GGGCTGCTGG CGCTGCTGGA TGAGGAGCAG	1200
CTCTGGGCCG AAGTGTGCGA GGCCGGGACC GTCCTGGACA GCAACCACAC GGTGGGCGTC	1260
CTGGCCAGCG CCCACCGCCC CCAGGGCCCG GCCGACGCCT GGCAGCGCCG GGTGCTGATC	1320

TACGCGAGCG ACGACACCCG CGCCACCCC AACCGCAGCG TCGCGGTGAC CCTGCGGCTG 1380
 CGCGGGGTGC CCCCCGGCCC GGGCCTGGTC TACGTCACGC GCTACCTGGA CAACGGGCTC 1440
 TGCAGCCCCG ACGGCGAGTG GCGGCGCCTG GGCCGGCCCG TCTTCCCCAC GGCAGAGCAG 1500
 TTCCGGCGCA TGCGCGCGGC TGAGGACCCG GTGGCCGCGG CGCCCCGCCC CTTACCCGCC 1560
 GGCGGCCGCC TGACCCTGCG CCCC GCGCTG CGGCTGCCGT CGCTTTTGCT GGTGCACGTG 1620
 TGTGCGCGCC CCGAGAAGCC GCCCGGGCAG GTCACGCGGC TCCGCGCCCT GCCCCTGACC 1680
 CAAGGGCAGC TGGTTCTGGT CTGGTCGGAT GAACACGTGG GCTCCAAGTG CCTGTGGACA 1740
 TACGAGATCC AGTTCTCTCA GGACGGTAAG GCGTACACCC CGGTCAGCAG GAAGCCATCG 1800
 ACCTTCAACC TCTTTGTGTT CAGCCAGAC ACAGGTGCTG TCTCTGGCTC CTACCGAGTT 1860
 CGAGCCCTGG ACTACTGGGC CCGACCAGGC CCCTTCTCGG ACCCTGTGCC GTACCTGGAG 1920
 GTCCCTGTGC CAAGAGGGCC CCCATCCCCG GGCAATCCAT GAGCCTGTGC TGAGCCCCAG 1980
 TGGGTTGCAC CTCCACCGGC AGTCAGCGAG CTGGGGCTGC ACTGTGCCCA TGCTGCCCTC 2040
 CCATCACCCC CTTTGCAATA TATTTTT 2067

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 653 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser
 1 5 10 15
 Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val
 20 25 30
 His Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg
 35 40 45
 Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr
 50 55 60
 Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val
 65 70 75 80
 Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu
 85 90 95
 Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr
 100 105 110
 His Leu Asp Gly Thr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro
 115 120 125
 Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu
 130 135 140

Asp	Lys	Gln	Gln	Val	Phe	Glu	Trp	Lys	Asp	Leu	Val	Ser	Ser	Leu	Ala	
145					150					155					160	
Arg	Arg	Tyr	Ile	Gly	Arg	Tyr	Gly	Leu	Ala	His	Val	Ser	Lys	Trp	Asn	
				165					170						175	
Phe	Glu	Thr	Trp	Asn	Glu	Pro	Asp	His	His	Asp	Phe	Asp	Asn	Val	Ser	
			180					185					190			
Met	Thr	Met	Gln	Gly	Phe	Leu	Asn	Tyr	Tyr	Asp	Ala	Cys	Ser	Glu	Gly	
		195					200					205				
Leu	Arg	Ala	Ala	Ser	Pro	Ala	Leu	Arg	Leu	Gly	Gly	Pro	Gly	Asp	Ser	
	210					215					220					
Phe	His	Thr	Pro	Pro	Arg	Ser	Pro	Leu	Ser	Trp	Gly	Leu	Leu	Arg	His	
225					230					235					240	
Cys	His	Asp	Gly	Thr	Asn	Phe	Phe	Thr	Gly	Glu	Ala	Gly	Val	Arg	Leu	
				245					250					255		
Asp	Tyr	Ile	Ser	Leu	His	Arg	Lys	Gly	Ala	Arg	Ser	Ser	Ile	Ser	Ile	
			260					265						270		
Leu	Glu	Gln	Glu	Lys	Val	Val	Ala	Gln	Glu	Ile	Arg	Gln	Leu	Phe	Pro	
		275					280					285				
Lys	Phe	Ala	Asp	Thr	Pro	Ile	Tyr	Asn	Asp	Glu	Ala	Asp	Pro	Leu	Val	
	290					295					300					
Gly	Trp	Ser	Leu	Pro	Gln	Pro	Trp	Arg	Ala	Asp	Val	Thr	Tyr	Ala	Ala	
305					310					315					320	
Met	Val	Val	Lys	Val	Ile	Ala	Gln	His	Gln	Asn	Leu	Leu	Leu	Ala	Asn	
				325					330					335		
Thr	Thr	Ser	Ala	Phe	Pro	Tyr	Ala	Leu	Leu	Ser	Asn	Asp	Asn	Ala	Phe	
			340				345						350			
Leu	Ser	Tyr	His	Pro	His	Pro	Phe	Ala	Gln	Arg	Thr	Leu	Thr	Ala	Arg	
		355					360					365				
Phe	Gln	Val	Asn	Asn	Thr	Arg	Pro	Pro	His	Val	Gln	Leu	Leu	Arg	Lys	
	370					375					380					
Pro	Val	Leu	Thr	Ala	Met	Gly	Leu	Leu	Ala	Leu	Leu	Asp	Glu	Glu	Gln	
385					390					395					400	
Leu	Trp	Ala	Glu	Val	Ser	Gln	Ala	Gly	Thr	Val	Leu	Asp	Ser	Asn	His	
				405					410					415		
Thr	Val	Gly	Val	Leu	Ala	Ser	Ala	His	Arg	Pro	Gln	Gly	Pro	Ala	Asp	
			420					425					430			
Ala	Trp	Arg	Ala	Ala	Val	Leu	Ile	Tyr	Ala	Ser	Asp	Asp	Thr	Arg	Ala	
		435					440					445				
His	Pro	Asn	Arg	Ser	Val	Ala	Val	Thr	Leu	Arg	Leu	Arg	Gly	Val	Pro	
	450					455					460					
Pro	Gly	Pro	Gly	Leu	Val	Tyr	Val	Thr	Arg	Tyr	Leu	Asp	Asn	Gly	Leu	
465					470					475					480	
Cys	Ser	Pro	Asp	Gly	Glu	Trp	Arg	Arg	Leu	Gly	Arg	Pro	Val	Phe	Pro	
				485					490					495		
Thr	Ala	Glu	Gln	Phe	Arg	Arg	Met	Arg	Ala	Ala	Glu	Asp	Pro	Val	Ala	

500	505	510
Ala Ala Pro Arg Pro Leu Pro 515	Ala Gly Gly Arg Leu 520	Thr Leu Arg Pro 525
Ala Leu Arg Leu Pro Ser Leu 530	Leu Leu Val His Val 535	Cys Ala Arg Pro 540
Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr 545	550	555
Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys 565	570	575
Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr 580	585	590
Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser 595	600	605
Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp 610	615	620
Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu 625	630	635
Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro 645	650	

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCCTATGCTG AGCACAAGTT ACAG

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Complementary sequence of a PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCCCTTGAGC TCGTCACTGG CGACGCCACA GGTA

34